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OW protein - protein search, using sw model

Run on: December 19, 2002, 14:53:27 ; Search time 22 Seconds  
(without alignments)  
2482.016 Million cell updates/sec

Title: US-08-813-323b-2

Perfect score: 3008

Sequence: 1 MESSKKMDSFGALQTNPPK.....IKDDTIFVYVDTSDLPDP 568

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : PIR.73:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3008	100.0	568	2	A55960 CD40 receptor-asso
2	2886.5	96.0	567	2	A49272 CD40 receptor-asso
3	2839.5	94.4	543	2	S68467 CD40 receptor-asso
4	1192.5	39.6	557	2	JC6539 tumor necrosis fac
5	837.5	27.8	501	2	T61512 TNF receptor assoc
6	811	27.0	501	2	S56163 tumor necrosis fac
7	636.5	21.2	416	2	B55649 TNF-associated pr
8	628	20.9	409	2	A54750 TNF receptor assoc
9	560.5	18.6	470	2	I38026 MLN 62 protein - h
10	552	18.4	522	2	S71821 probable interleuk
11	522.5	17.4	509	2	T22238 hypothetical prote
12	201	6.7	458	2	A29361 DG17 protein - sll
13	173.5	5.8	313	2	B96692 hypothetical prote
14	159	5.3	634	2	I49642 nuclear phosphopro
15	152.5	5.1	609	2	A43906 meprin A (EC 3.4.2
16	151.5	5.0	704	2	A48040 CG1 protein - huma
17	150.5	5.0	1300	2	I53799 hypothetical prote
18	150	5.0	1005	2	A64465 hypothetical prote
19	149.5	5.0	919	2	B72765 hypothetical prote
20	148.5	4.9	1085	2	F96712 hypothetical prote
21	148	4.9	1676	2	E71410 probable centromer
22	148	4.9	1957	2	T38077 hypothetical colle
23	147.5	4.9	1356	2	S32763 kinectin 1 - human
24	146	4.9	1039	2	S18199 myosin heavy chain
25	145.5	4.8	1218	2	T14265 golgin-245 - mouse
26	145.5	4.8	1577	2	T19722 hypothetical prote
27	145	4.8	1679	2	S48385 hypothetical prote
28	144.5	4.8	1104	2	I38869 transcription fact
29	144	4.8	1727	2	T50073 myosin-like coiled

30	143.5	4.8	852	2	D72230 conserved hypothet
31	143	4.8	698	2	S52696 myosin heavy chain
32	142.5	4.7	1313	2	P96673 hypothetical prote
33	142	4.7	2253	2	T30336 nuclear/mitotic ap
34	141.5	4.7	412	2	D88072 protein ZK1240.1
35	141.5	4.7	1690	2	T13030 microtubule bindin
36	141	4.7	879	2	C71083 conserved hypothet
37	141	4.7	1046	2	A66790 ATP-dependent dsDN
38	141	4.7	1940	1	A24922 myosin heavy chain
39	139.5	4.6	512	2	F66193 hypothetical prote
40	139.5	4.6	631	2	UC4298 hyaluronan recepto
41	139.5	4.6	1164	2	T24806 hypothetical prote
42	139	4.6	551	2	JC7562 glioblastoma RING
43	138	4.6	1187	2	T18355 hypothetical prote
44	137.5	4.6	1607	2	T43212 insulin-like growt
45	137	4.6	886	2	H63378 conserved hypothet

## ALIGNMENTS

## RESULT 1

A55960  
CD40 receptor-associated factor 1 - human  
N:Alternate names: CD40-binding protein  
C:Species: Homo sapiens (man)  
C>Date: 15-Mar-1996 #sequence, revision 15-Mar-1996 #text, change 01-Dec-2000  
C:Accession: A55960; A55649; A55135  
R:Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.  
Science 267, 1494-1498, 1995  
A:Title: Involvement of CRAF1, a relative of TRAF, in CD40 signaling.  
A:Reference number: A55960; MUID:95184010; PMID:7533327  
A:Accession: A55960  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-568 <RES>  
A:Cross-references: EMBL:021092; NID:9726087; PIDN:AA50112.1; PID:9726088  
R:Mosialos, G.; Birkenbach, M.; Yalamanchili, R.; VandeSalle, T.; Ware, C.; Kieff, E.  
Cell 80, 389-399, 1995  
A:Title: The Epstein-Barr virus transforming protein Lmp1 engages signaling proteins  
A:Reference number: A55649; MUID:95163092; PMID:7859281  
A:Accession: A55649  
A>Status: not shown  
A:Molecule type: mRNA  
A:Residues: 1-128, 'W', 130-568 <MOS>  
A:Cross-references: GB:019260; NID:9675459; PIDN:AA65732.1; PID:9675460  
R:Hu, H.M.; O'Rourke, K.; Boguski, M.S.; Dixit, V.M.  
J. Biol. Chem. 269, 30069-30072, 1994  
A:Title: A novel RING finger protein interacts with the cytoplasmic domain of CD40.  
A:Reference number: A55135; MUID:95073988; PMID:7527023  
A:Accession: A55135  
A>Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-128, 'W', 130-133, 135-404, 'G', 406-568 <HUA>  
A:Cross-references: GB:015637; NID:9595910; PIDN:AA56753.1; PID:9595911  
C:Genetics:  
A:Gene: CRAF1  
C:Superfamily: CD40 receptor-associated protein GAP-1; RING finger homology  
C:Keywords: coiled coil; zinc  
F:49-97/Domain: RING finger homology <RING>

Query Match 100.0%; Score 3008; DB 2; Length 568;  
Best Local Similarity 100.0%; Pred. No. 9, 6e-167;  
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MESSKKMDSFGALQTNPPKLTHTDSAGTPVFPVPGGKKEFKYTVEDKKYCKECHLV 60  
DB 1 MESSKKMDSFGALQTNPPKLTHTDSAGTPVFPVPGGKKEFKYTVEDKKYCKECHLV 60  
QY 61 CSPKQTEGCHRFCECSMALSSSPKCTACQESIVKDKVFRDNCCKREILALQIYCRNE 120  
DB 61 CSPKQTEGCHRFCECSMALSSSPKCTACQESIVKDKVFRDNCCKREILALQIYCRNE 120

QY 121 SRGCAEQLTLGLHLVHLKNDCHFEELPCVPRDCKEKLKRDLDHYEAKCYREATCSHC 180  
 |||||  
 Db 121 SRGCAEQLTLGLHLVHLKNDCHFEELPCVPRDCKEKLKRDLDHYEAKCYREATCSHC 180  
 QY 181 KSOVPMIALOKHEDTDCPCVVVSCPHKCSVOITLRLSELSEHLSECVNAPSTCSFKRYGCV 240  
 |||||  
 Db 181 KSOVPMIALOKHEDTDCPCVVVSCPHKCSVOITLRLSELSEHLSECVNAPSTCSFKRYGCV 240  
 QY 241 FOGTNOQIKAHFASAVOHVNLKEMNSLEKRVSLQNESVEKNKSIOSLHNOICSEFI 300  
 |||||  
 Db 241 FOGTNOQIKAHFASAVOHVNLKEMNSLEKRVSLQNESVEKNKSIOSLHNOICSEFI 300  
 QY 301 EIEROKEMLRNNESKILHLQVVIDSOAEKLELDEIRPFROOMEADSMKSSVESLQNR 360  
 |||||  
 Db 301 EIEROKEMLRNNESKILHLQVVIDSOAEKLELDEIRPFROOMEADSMKSSVESLQNR 360  
 QY 361 VTELESVDKSAGQVARNRTGLLESQLSRHDQMLSVHDIRLADMRLRFVLETASYNGVLIW 420  
 |||||  
 Db 361 VTELESVDKSAGQVARNRTGLLESQLSRHDQMLSVHDIRLADMRLRFVLETASYNGVLIW 420  
 QY 421 KIRDYKRRKQEAVMGKTLISYQPFYTGFGYKMCARVYLNGDMGKGTLSLFFVIMRG 480  
 |||||  
 Db 421 KIRDYKRRKQEAVMGKTLISYQPFYTGFGYKMCARVYLNGDMGKGTLSLFFVIMRG 480  
 QY 481 EYDALLPMPFKOKVTLMLMDQSSRRHLGDAFKPDPNSSSEFKKPTGEMNIASGCPVFAO 540  
 |||||  
 Db 481 EYDALLPMPFKOKVTLMLMDQSSRRHLGDAFKPDPNSSSEFKKPTGEMNIASGCPVFAO 540  
 QY 541 TVLENGTYIKDITFIKIVIVTSDLPDP 568  
 |||||  
 Db 541 TVLENGTYIKDITFIKIVIVTSDLPDP 568

## RESULT 2

CD40 receptor-associated factor 1 - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 15-Mar-1996 #sequence\_revision 15-Mar-1996 #text\_change 18-Aug-2000  
 C:Accession: I49272  
 R:Cheng, G.; Cleary, A.M.; Ye, Z.S.; Hong, D.I.; Lederman, S.; Baltimore, D.  
 Science 267, 1494-1498, 1995  
 A:Title: Involvement of GRAF1, a relative of TRAF, in CD40 signaling.  
 A:Reference number: A55960; MUID:95184010; PMID:7533327  
 A:Accession: I49272  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-567 <RES>  
 A:Cross-references: EMBL:U21050; NID:g719292; PIDN:AAC52175.1; PID:g719293  
 C:Genetics:  
 A:Gene: GRAF1  
 C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology  
 C:Keywords: zinc finger  
 F:48-96/Domain: RING finger homology <RNG>

Query Match 96.0%; Score 2886.5; DB 2; Length 567;  
 Best Local Similarity 96.1%; Pred. No. 1e-159;  
 Matches 546; Conservative 7; Mismatches 14; Indels 1; Gaps 1;  
 QY 1 MESSKKMDSFGALQTNPLKLTDRSAGTPVFPDGGKKEKFTVTEDEKTKCEKCHLYL 60  
 |||||  
 Db 1 MESSKKMDSFGALQTNPLKLTDRSAGTPVFPDGGKKEKFTVTEDEKTKCEKCHLYL 60  
 QY 61 CSPKQTECHGRFCESMAALLSSSSPKTACQESIVYKDKFKNCKCKREILALQIYCRNE 120  
 |||||  
 Db 61 CSPKQTECHGRFCESMAALLSSSSPKTACQESIVYKDKFKNCKCKREILALQIYCRNE 120  
 QY 121 SRGCAEQLTLGLHLVHLKNDCHFEELPCVPRDCKEKLKRDLDHYEAKCYREATCSHC 180  
 |||||  
 Db 121 SRGCAEQLTLGLHLVHLKNDCHFEELPCVPRDCKEKLKRDLDHYEAKCYREATCSHC 180  
 QY 181 KSOVPMIALOKHEDTDCPCVVVSCPHKCSVOITLRLSELSEHLSECVNAPSTCSFKRYGCV 240  
 |||||  
 Db 181 KSOVPMIALOKHEDTDCPCVVVSCPHKCSVOITLRLSELSEHLSECVNAPSTCSFKRYGCV 240

QY 241 FOGTNOQIKAHFASAVOHVNLKEMNSLEKRVSLQNESVEKNKSIOSLHNOICSEFI 300  
 |||||  
 Db 241 FOGTNOQIKAHFASAVOHVNLKEMNSLEKRVSLQNESVEKNKSIOSLHNOICSEFI 300  
 QY 301 EIEROKEMLRNNESKILHLQVVIDSOAEKLELDEIRPFROOMEADSMKSSVESLQNR 360  
 |||||  
 Db 301 EIEROKEMLRNNESKILHLQVVIDSOAEKLELDEIRPFROOMEADSMKSSVESLQNR 360  
 QY 361 VTELESVDKSAGQVARNRTGLLESQLSRHDQMLSVHDIRLADMRLRFVLETASYNGVLIW 420  
 |||||  
 Db 361 VTELESVDKSAGQVARNRTGLLESQLSRHDQMLSVHDIRLADMRLRFVLETASYNGVLIW 420  
 QY 421 KIRDYKRRKQEAVMGKTLISYQPFYTGFGYKMCARVYLNGDMGKGTLSLFFVIMRG 480  
 |||||  
 Db 421 KIRDYKRRKQEAVMGKTLISYQPFYTGFGYKMCARVYLNGDMGKGTLSLFFVIMRG 480  
 QY 481 EYDALLPMPFKOKVTLMLMDQSSRRHLGDAFKPDPNSSSEFKKPTGEMNIASGCPVFAO 540  
 |||||  
 Db 481 EYDALLPMPFKOKVTLMLMDQSSRRHLGDAFKPDPNSSSEFKKPTGEMNIASGCPVFAO 540  
 QY 541 TVLENGTYIKDITFIKIVIVTSDLPDP 568  
 |||||  
 Db 541 TVLENGTYIKDITFIKIVIVTSDLPDP 568

## RESULT 3

CD40 receptor-associated protein CAP-1 - human  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 08-Dec-2000  
 C:Accession: S68467; 153498  
 R:Sato, T.; Irie, S.; Reed, J.C.  
 FEBS Lett. 358, 113-118, 1995  
 A:Title: A novel member of the TRAF family of putative signal transducing proteins b1  
 A:Reference number: I53498; MUID:95129692; PMID:7530216  
 A:Status: nucleic acid sequence not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-543 <SAT>  
 A:Cross-references: EMBL:L38509; NID:g695357; PIDN:AAA68195.1; PID:g695358  
 A:Experimental source: t15sue-type fetal brain  
 C:Genetics:  
 A:Gene: CAP-1  
 C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology  
 C:Keywords: homodimer; signal transduction; zinc finger  
 F:49-97/Domain: RING finger homology <RNG>

Query Match 94.4%; Score 2839.5; DB 2; Length 543;  
 Best Local Similarity 95.4%; Pred. No. 5.1e-157;  
 Matches 542; Conservative 0; Mismatches 1; Indels 25; Gaps 1;  
 QY 1 MESSKKMDSFGALQTNPLKLTDRSAGTPVFPDGGKKEKFTVTEDEKTKCEKCHLYL 60  
 |||||  
 Db 1 MESSKKMDSFGALQTNPLKLTDRSAGTPVFPDGGKKEKFTVTEDEKTKCEKCHLYL 60  
 QY 61 CSPKQTECHGRFCESMAALLSSSSPKTACQESIVYKDKFKNCKCKREILALQIYCRNE 120  
 |||||  
 Db 61 CSPKQTECHGRFCESMAALLSSSSPKTACQESIVYKDKFKNCKCKREILALQIYCRNE 120  
 QY 121 SRGCAEQLTLGLHLVHLKNDCHFEELPCVPRDCKEKLKRDLDHYEAKCYREATCSHC 180  
 |||||  
 Db 121 SRGCAEQLTLGLHLVHLKNDCHFEELPCVPRDCKEKLKRDLDHYEAKCYREATCSHC 180  
 QY 181 KSOVPMIALOKHEDTDCPCVVVSCPHKCSVOITLRLSELSEHLSECVNAPSTCSFKRYGCV 240  
 |||||  
 Db 181 KSOVPMIALOKHEDTDCPCVVVSCPHKCSVOITLRLSELSEHLSECVNAPSTCSFKRYGCV 240  
 QY 241 FOGTNOQIKAHFASAVOHVNLKEMNSLEKRVSLQNESVEKNKSIOSLHNOICSEFI 300  
 |||||  
 Db 241 FOGTNOQIKAHFASAVOHVNLKEMNSLEKRVSLQNESVEKNKSIOSLHNOICSEFI 300  
 QY 301 EIEROKEMLRNNESKILHLQVVIDSOAEKLELDEIRPFROOMEADSMKSSVESLQNR 360  
 |||||

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Db 276 EIERKEKRLNNESKTLHLQVHDSQAKKLELDEKELSFQNNBEADSMKSSVESLQNR 335
      |||
Oy 361 VTELESVDKSGAVARNTGLLESQLSRRHDMLSVHDRLADMDLRFVLETASTYNGVLTW 420
      |||
Db 336 VTELESVDKSGAVARNTGLLESQLSRRHDMLSVHDRLADMDLRFVLETASTYNGVLTW 395
      |||
Oy 421 KIRYKRRKQEAVMGKTSLSYQPFYTGFGYKMCARVYLLGDGKGKTHLSLFFVIMRG 480
      |||
Db 396 KIRYKRRKQEAVMGKTSLSYQPFYTGFGYKMCARVYLLGDGKGKTHLSLFFVIMRG 455
      |||
Oy 481 EVDALLPMPFKOKVTLMMDGSSRRHLGDAFPDPNSSSEFKKPTGENNIAAGCPVEVAQ 540
      |||
Db 456 EVDALLPMPFKOKVTLMMDGSSRRHLGDAFPDPNSSSEFKKPTGENNIAAGCPVEVAQ 515
      |||
Oy 541 TVLENGTYIKDDTIFIKVYVDTSDLPDP 568
      |||
Db 516 TVLENGTYIKDDTIFIKVYVDTSDLPDP 543
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## RESULT 4

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Jc6539
tumor necrosis factor receptor-associated factor 5 homolog - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 18-Aug-2000
C:Accession: Jc6539
R:Mizushima, S.; Fujita, M.; Ishida, T.; Azuma, S.; Kato, K.; Hirai, M.; Otsuka, M.; Yan
Gene 207, 135-140, 1998
A:Title: Cloning and characterization of a cDNA encoding the human homolog of tumor necr
A:Reference number: Jc6539; MUID:98172745; PMID:9511754
A:Accession: Jc6539
A:Molecule type: mRNA
A:Residues: 1-357 <M12>
A:Cross-references: DBJ:AB000509; NID:92982670; PIND:BA25262.1; PID:92982671
C:Comment: This protein is involved in transduction of signals from various tumor necros
mphtoxin-beta receptor.
C:Genetics:
A:Map position: 1q32.3-1q41.1
C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
C:Keywords: coiled coil; tumor; zinc finger
F:41-90/Domain: RING finger homology <RNG>

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Query Match 39.6% Score 1192.5; DB 2; Length 557;
Best Local Similarity 42.0% Pred. No. 9; 9e-62;
Matches 222; Conservative 121; Mismatches 178; Indels 21; Gaps 9;

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Oy 25 RSAGTPEVPEDEGGYKEKFKYKVEYKCEKCHLVLCSPKOTEGHRCFESCMALLS-S 83
      |||
Db 17 QNSGNSISLDFERSIEQVEFERLEERYKCAFCHSVLHNPHTQCGHRFCOCHLSIRELN 76
      |||
Oy 84 SSKPCTACOSIYKDKVFKNCKKRETLAQITCRNESRGCAGQLLGLHVLKNDCH 143
      |||
Db 77 TVPICPVDEKIVISOEFKQKCNCKREVLNLYVCSN-APCCNAKVLIGRYODHLQ-QCLE 134
      |||
Oy 144 EELPCVAPDCKEYLRKDLRDHYEAKCYREATCSHCKSQVPMIALQKHEDTDCPCVVVS 203
      |||
Db 135 QPVOCSMEKREPVLRDLDEKHLASQCFKREKCLVKAKVYVYINQNHENLCPREPV 194
      |||
Oy 204 CPHKCVQTLRLSELNHLSECVNASTCSTCFKRYGCVFQSTNOQIKAHKSSAVQVNL 263
      |||
Db 195 CPNNCA-KILKTEVEVDHLVCPAEEDCPFKHYGCAYVTDKRRNLQHHESALREHRLV 253
      |||
Oy 264 KEMNSLSLEKVVYLLQNSVSKNKSIOGLHNOCSFEIEIRKEMLNKNSKTLHLQRYL 323
      |||
Db 254 LEKVVQLEBQISDLHKLSEKSTIQQLAETIKLEKEFPQFOLRPGKNSFLPNQ-VP 312
      |||
Oy 324 DSAEKLKELDKETIRPE-----RQNNBEADSMKSSVESLQNRVTELESVDKSGAVARNT 377
      |||
Db 313 ASHIDKSNMLEAQVHQLQWNOONKFDRPLMEAVDIYKOKITLLEND-----QR 365
      |||
Oy 378 TGLLESQLSRRHDMLSVHDRLADMDLRFVLETASTYNGVLTIRYKRRKQEAVMGK 437
      |||
Db 366 LAVLEETNKHDTIHINIKHQAQSKNEERFKLLBGTCTYNGKLIMKVDTYDKMKREAVDGH 425
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Oy 438 ISLYSOPFYNGFYKMCARVYLLGDGKGKTHLSLFFVIMRGEXDALLPMPFKOKVTLM 497
      |||
Db 426 VSFISQSFYTSRCGRYLCARVYLLGDGSGRSHLSLFFVIMRGREFSILQMPFRQAVTLM 485
      |||
Oy 498 LMDGSSRRHLGDAFPDPNSSSEFKKPTGENNIAAGCPVEVAQVLEN--GTIYKDDTIF 555
      |||
Db 486 LLDQ-SGKKNIMETFKPDPNSSSEFKKPTGENNIAAGCPVEVAQVLENKNAVYKDDTIF 544
      |||
Oy 556 IKVYVDTSDLPDP 567
      |||
Db 545 LKVAVDLTLDLED 556
      |||

```

## RESULT 5

```

I61512
TNF receptor associated factor 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 18-Aug-2000
C:Accession: I61512
R:Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.
Cell 78, 681-692, 1994
A:Title: A novel family of putative signal transducers associated with the cytoplasmic
A:Reference number: A54750; MUID:94349371; PMID:8069916
A:Accession: I61512
A:Status: preliminary; translated from GB/EMBL/DDAJ
A:Molecule type: mRNA
A:Residues: 1-501 <R5>
A:Cross-references: GB:J35303; NID:9532620; PIND:AAC37662.1; PID:9532621
C:Genetics:
A:Gene: TNFA2
C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology
C:Keywords: zinc
F:30-78/Domain: RING finger homology <RNG>

```

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Query Match 27.8% Score 837.5; DB 2; Length 501;
Best Local Similarity 33.6% Pred. No. 3e-41;
Matches 196; Conservative 89; Mismatches 194; Indels 105; Gaps 17;

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Oy 3 SSKKNDSPGALQTNPLKLTHTDRSAGRPVFPEDEGGYKEKFKVT-VEDKYKCEKCHLVLC 61
      |||
Db 2 AAAYTSFGSLLELP-----GFSKTLGLTRLEKAYLCSCNKNILR 42
      |||
Oy 62 SPKQTECHRCESCMALLSSSPKCTAC-----QEST--VKDKYKDNCKKRETLA 112
      |||
Db 43 RPFQAGCHRCSPCLTSLTSGPNCAACYEGLYEGISILSSSAFPDNNARRREVES 102
      |||
Oy 113 LQITRNRSRGAEDLTGLHVLNHLKNDCHFEELPCVPDCKEYLRKDLRDHYEAKCY 172
      |||
Db 103 LPVACPND--GCTWKGTLKEYESCHGCLPPLTEC--PACKGLVRLSEKHHTEDQCPK 158
      |||
Oy 173 REATSHCKSGVPMIALQKHEDTDCPCVVVSCPHKCSVQTLRLSELNHLSECVNASTC 232
      |||
Db 159 KSLSCONCHRAPSHVDLEHYHY-CRKRPLTC-DCCGKKIIRPRETFQDHVNAAGSCRYLC 216
      |||
Oy 233 SPKRYGCVFQSTNOQIKAHKSSAVQVNLKEMNSLSLEKVS-----LLQNSV 282
      |||
Db 217 RFTVGCSEMEVETENLOHLEQRLREHLL--LSFLEAQSPGTLNQVRELLQRCOI 274
      |||
Oy 283 EKNKSIQSLHNOCSFEIEIRKEMLNKNSKTLHLQRYVDSQAEKLKELDKETIRPRQ 342
      |||
Db 275 LEOK-TAFETNVCVUNRVER-----VAVTAECSSRQHRDQD----- 312
      |||
Oy 343 NNEEADSMKSSVESLQNRVTELESVDKSGAVARNTGLLESQLSRRHDMLSVHDRLADM 402
      |||
Db 313 -----KTEALSNNKVOGLE-----RSIGL-----KDLAMADL 338
      |||
Oy 403 DLRFVLETASTYNGVLTIRYKRRKQEAVMGKTSLSYQPFYTGFGYKMCARVYLLNG 462
      |||
Db 339 EOKVSELEVTYDGVETWISDFTRRQDAVAGTRPALFSPFVTSRYGKMCLEVYLLNG 398
      |||
Oy 463 DGMGKTHLSLFFVIMRGEXDALLPMPFKOKVTLMMDGSSRRHLGDAFPDPNSSSEFK 522
      |||

```

Db 399 DGTGRGTHLSLFVVMKGPNDALLQWPNQKVTLLMDH-NNREHVIDAFRPDYTSFQ 457  
 QY 523 KPTGEMNIASGCPVEVAQTVLE-NGEYIKDDTFIKYIVTSD 565  
 Db 458 RPSVDMINIASGCPLEFCVSKMEAKNSYKDDALFIRKATVDLTGL 501

## RESULT 6

556163

tumor necrosis factor type 2 receptor associated protein - human

N:Alternate names: TNF receptor-associated protein

C:Species: Homo sapiens (man)

C&gt;Date: 10-Oct-1995 #sequence\_revision 01-Dec-1995 #text-change 03-Nov-2000

C:Accession: S56163; S58925; S58926; I38729

R:Song, H.Y.; Donner, D.B.

Biochem. J. 309, 825-829, 1995

A:Title: Association of a RING finger protein with the cytoplasmic domain of the human

A:Reference number: S56163; MUID:95366958; PMID:7639698

A:Accession: S56163

A:Molecule type: mRNA

A:Residues: 1-501 &lt;SON1&gt;

A:Cross-references: EMBL:U12597; NID:g975272

R:Song, H.Y.; Donner, D.

Submitted to the EMBL Data Library, July 1994

A:Description: Association of a RING finger protein with the cytoplasmic domain of the h

A:Reference number: S58925

A:Accession: S58925

A:Molecule type: mRNA

A:Residues: 1-42,63-342,363-501 &lt;SON2&gt;

A:Cross-references: EMBL:U12597; NID:g975272

A:Accession: S58926

A:Molecule type: mRNA

A:Residues: 1-342, RPPQAGCGHRYCSFCLASIL', 363-501 &lt;SON3&gt;

A:Cross-references: EMBL:U12597; NID:g975272; PIDN:AAA87706.1; PID:g975273

R:Rothe, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.

Cell 78, 681-692, 1994

A:Title: A novel family of putative signal transducers associated with the cytoplasmic d

A:Reference number: A54750; MUID:9449371; PMID:8069916

A:Accession: I38729

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-342, RPPQAGCGHRYCSFCLASIL', 363-501 &lt;ROT&gt;

A:Cross-references: EMBL:U12597; NID:g975272; PIDN:AAA87706.1; PID:g975273

C:Genetics:

A:Gene: GDB:TRAF2; TRAF

A:Cross-references: GDB:6268629; OMIM:601895

A:Map position: 9q34-q34

C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology

C:Keywords: zinc finger

F:30-78/Domain: RING finger homology &lt;RNG&gt;

Query Match 27.0%; Score 811; DB 2; Length 501;

Best Local Similarity 35.2%; Pred. No. 1e-39;

Matches 196; Conservative 86; Mismatches 177; Indels 98; Gaps 21;

QY 36 OGGYEKEFKYT-VEDKYCEKHLYLCPKQECGHRFCESMALLSSSPKCTAC-OE 93  
 Db 16 QGFSKTLTGTRLEAKYLCASACRYLRRPQAGCGHRYCSFCLASILSSGPNCAACVHE 75  
 QY 94 SLVKDV-----FKDNCKREILALQIYCRNESRGACALDTGHLVLKNDCHTEE 145  
 Db 76 GYIEGISTLESSAFPPNARREYESLPVC--PSDCTMKGLTKER-----ESCHGR 128  
 QY 146 LPCVR---PDCKEYLRKLDLNDHVEKACKYREAFCSHCKSGVPMIALQKHEDTDCPCVV 202  
 Db 129 CPLMLTECPACKGLVRLGEKERHLEHECPERSLSCRHRCAPCCGADVKAHNEV-CPRKPL 187  
 QY 203 SCPRKSGVOTLLRSELASHLSECVNAPSTCSFKRYGC--FQGNQOTKAHEASSAYOHV 260  
 Db 188 TC-DGCGKKKIPREKFDQHVKTGCKRVPCCFHAIGLETVEGKKQ--EHEVOMLRHLL 244  
 QY 261 NLKEMWSLEKK-----VSLQN-ESVEKNKSIOSLHNOQCSFEIEIRKREML 309

Db 245 AML--LSSVLEAKPPLGDSHAGSELLQCBSELEKTA--TFENAVYNREVER----- 295  
 QY 310 RNNSEKILHLQRYDSQAEKLEKDEIRPFQNNWEADSMKSSVESLQNRTELESYDK 369  
 Db 296 -----VANTAEACS-----RQHRLLDD--KTEALSNKYQOLE----- 325  
 QY 370 SAGQVARNRGLLESQSLSRDQMLSYHDIRLMDIRFOVLETAISNGVLYMKIRDYKRR 429  
 Db 326 -----RSIGL-----KDLAMADLEQKVLMEASTYDGVFIKISDFPRKL 365  
 QY 430 QEAVMGKTLISYQPFYTGFGYKMCARVYVYNGDMGKGTLSLFPYIMRGEYDALLPWP 489  
 Db 366 QEAVAGRIPIRSPAPFYSRYGYKMCRLIYNGDGTGTHLSLFVVMKGPNDALLRMP 425  
 QY 490 FKQKTYLMDGSSRRHLGDAFKDPNPSKFKTKPTGEMNIASGCPVEVAQTVLE-NGTY 548  
 Db 426 FQKQKTYLMDLQ-NNREHVIDAFRPDYTSFQ-RPSVDMINIASGCPLEFCVSKMEAKNSY 484  
 QY 549 IKDDTFIKYIVTSD 565  
 Db 485 VRDDAIFIRKATVDLTGL 501

## RESULT 7

B55649

TNFR-associated protein EB16 - human

C:Species: Homo sapiens (man)

C&gt;Date: 23-Mar-1995 #sequence\_revision 23-Mar-1995 #text-change 08-Oct-1999

C:Accession: B55649

R:Mostafaei, G.; Birkenbach, M.; Yalamanchili, R.; Vanarsdale, T.; Ware, C.; Kieff, E.

Cell 80, 389-399, 1995

A:Title: The Epstein-Barr virus transforming protein LMP1 engages signaling proteins

A:Reference number: A55649; MUID:95163092; PMID:7859281

A:Accession: B55649

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-416 &lt;MOS&gt;

A:Cross-references: GB:U19261; NID:g675461; PIDN:AAA62309.1; PID:g675462

Query Match 21.2%; Score 636.5; DB 2; Length 416;

Best Local Similarity 35.3%; Pred. No. 1e-29;

Matches 164; Conservative 72; Mismatches 126; Indels 103; Gaps 17;

QY 138 KNDCHFEELPCVRPDCKEYLRKDLRDHVEKACKYRATSTSHCKSGVPMIALQKHEDTDC 197  
 Db 15 ENERPFGCPPTVCGDPKRP-----RALCCAGCLSENP-----RNGEDQIC 54  
 QY 198 PCVYVSCPHKCSVOTL-----LRSELASHLSECVNAPSTCSFKRYGCVFQGTNQOIK 249  
 Db 55 P-----KCRGDLQSIISPGSRRLTQEKAN-PEVAEAGIGCPFAGVCGSPQSVQ 105  
 QY 250 AHEASSAVOHNL-----KEMS-----NSLEKKVSLQ-NESEVKNKSIO-SLH 292  
 Db 106 EHEVTSQTSHTLNLGKMKQWKARLGGCLSGPMALQNSIDQLQAAVEVAGDLEVDY 165  
 QY 293 NQICSEFIEIEROKEMLRNNSEKILHLQRYDSQAEKLEKDEIRPFQNNWEADSMK 352  
 Db 166 RAPCS-----ESQEE-----LALQHPM--KETLALBEKLVF-----E 198  
 QY 353 SVESLQNRVTELESYVDSACQVARNRGLLESQSLR-----DOMLSVHDIRLA 400  
 Db 199 NIVAVLNKEVE-----ASHLALATSIHQSLDRRIILSLQRYVELQOTLAQKQDALG 251  
 QY 401 DMDLRFOVLETAISNGVLYMKIRDYKRRQEAVMGTSLSQPFYTGFGYKMCARVYL 460  
 Db 252 KLEOSLRIMEASFDGTFMKLTITNVRCHESACGTFVLSFAFTAYAGKGLCLRLYL 311  
 QY 461 NGDMGKGTLSLFVYIMRGEYDALLPWPFKQKVTYLMMDGSSRRHLGDAFKDPNPS 520  
 Db 312 NGDGTGKRTLSLFYIMRGEYDALLPWPFRKNVTFTMLDQ--NNRHAIDARRPDLSSAS 370  
 QY 521 FKPTGEMNIASGCPVEVAQTVLE-NGTYIKDDTFIKYIVTSD 563

Db 371 FGRPQSENNVAGCPLFFPLSLKQSPKHAAYKDDTMFLKCIIVETS 415

# RESULT 8

A54750

TNF receptor associated factor 1 - mouse

C:Species: Mus musculus (house mouse)

C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999

C:Accession: A54750

R:Roche, M.; Wong, S.C.; Henzel, W.J.; Goeddel, D.V.

Cell 78, 681-692, 1994

A:Title: A novel family of putative signal transducers associated with the cytoplasmic

A:Reference number: A54750; MUID:94349374; PMID:8069916

A:Accession: A54750

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-409 <RES>

A:Cross-references: GB:L35302; NID:g532618; PIDN:AAC37663.1; PID:g532619

C:Genetics:

A:Gene: TRAF1

Query Match 20.9%; Score 628; DB 2; Length 409;  
Best Local Similarity 36.6%; Pred. No. 3.1e-29;  
Matches 154; Conservative 69; Mismatches 128; Indels 70; Gaps 13;

173 REATCSHCKSQVPMIALQKHEDTDCPCVYVSCPHKCSQVTLRLSELNSECYNAPSTC 232

Db 28 RVLCTACTLSE---NLNDEDDRICPCRADNLHPVSGSPLTQE-KVN-SDVAEALIMC 81

223 SFKRYGCVFGTNOQIKHAESSAVQHVNL---LKEWNS-----LEKKVSL 277

Db 82 PFAGVGCSEFKSPQSMQHEATSOSSHLYLLAVLKEKSSPGSNLSAPALERNISEL 141

278 QNESVEKNKSIQSLHNOICSEFEIEROKEMLRNNEKILHLQRYIDSQAEK-LKEIDKE 336

Db 142 Q-----LQAAVEATGDELVDCYRAPCESQEBELQHLVYK-----EKLQAELEK 186

337 IRRPQNMEDADSMKSSVESLONRYTELESVDKSGAVARNTGLLESLSR----- 388

Db 187 LRVF-----ANTVAVALNKEVE-----ASHLALASHIOSQLDREHLSLEOR 228

389 ----DOMLSVHDRLADMDLRFQVLETASYNGVLIWKIRYKRRKOAVMKTLSLQSP 444

Db 229 VVELQOTLAKQKQVGLKLEHSLRLMEASFGOTFLMKITNTVKRHESEVCRVTSLESPA 288

445 FTTGFTGKMCARVYLDGDMGKGTSLFVYINAGEEDALLPWFPRKQVYVLTMLMDQSS 504

Db 289 FTTAKYGYKLCLRLYLNDGSGKTHLSLFYIMGEVDALLPWFPRKQVYVLTMLMDQ-NN 347

505 RRLHLDAPDPNSSSFKKPTGEMNIASGCPVFAQVLEEN--GTYIKDDTIFIKVIVDT 562

Db 348 RERHLDARFDPDLSASFQRPQSENNVAGCPLFFPLSLKQSPKHAAYKDDTMFLKCIYDT 407

QY 563 S 563

Db 408 S 408

RESULT 9

138026

MLN 62 protein - human

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence\_revision 01-Nov-1996 #text\_change 02-Sep-2000

C:Accession: 138026; S60681

R:Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Matteil, M.G.; Chenard, M.P.; Lidereau, R.

Genomics 28, 367-376, 1995

A:Title: Identification of four novel human genes amplified and overexpressed in breast

A:Reference number: 137080; MUID:96039245; PMID:7490069

A:Accession: 138026

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-470 <RES>

A:Cross-references: EMBL:X80200; NID:g951276; PIDN:CAAS6491.1; PID:g951277

A:Note: submitted to the EMBL Data Library, July 1994

C:Genetics:

A:Gene: MLN62; CAPT1

C:Superfamily: CD40 receptor-associated protein CAP-1; RING finger homology

F;14-63/Domain: RING finger homology <RRN>

Query Match 18.6%; Score 560.5; DB 2; Length 470;  
Best Local Similarity 24.9%; Pred. No. 3e-25;  
Matches 147; Conservative 75; Mismatches 173; Indels 195; Gaps 13;

38 GYKEKVTVEEDYKCEKCHLVLCSPKQ--TEGHRPCECMAALLSSSPKCTACQESIV 96

Db 3 GFDFKFLERPKRRLCLPLCGKPRMEPVQVSTGCHRCDDTCLDFSEGVFKCPEDQLPMD 62

97 KQVFPDNCCKRIILALQYICRNESRCAGDQLTGLHLVNLNDCDFEELPCVRPD-CKE 155

Db 63 YAKIYDPPELEVQVGLPLRCHISEGCMNSGRLNLOGLH-NTCSFNVIQC--PRRCFM 119

156 KVLKDLRDHVEKACKYREATCSHCKSQVPMIALQKHE----- 193

Db 120 KLSRDLPLHLQHDPCPKRLKCEFCGCDPSGEAYESHGMCQDESYYCENKCGARMRGCL 179

194 -----DT-----DCPCVYVSCPHKCSQVTLRLSELNSECYNAPSTC 222

Db 180 LAQHATSECPKRPQCTYCTKEEFPTDIOSHQYOCPRPLVACPQCGVGTAVAREDLPGHL 239

223 SE-CVNAFSTCSFKRYGCVFGTNOQIKHAESSAVQHVNLKEMNSLEKKVSLQNES 281

Db 240 KDSQCNTRALVLCPRKDSGCKHRCPKLMARHVESVYRPLMM----- 281

282 VERKNKSIQSLHNOICSEFEIEROKEMLRNNEKILHLQRYIDSQAEK-LKEIDKEI 341

Db 282 -----CA-----LVSRQDELQELKREL----- 299

342 QNNEADSMKSSVESLONRYTELESVDKSGAVARNTGLLESLSRHDMLSHVDRLAD 401

Db 300 -----BELSV----- 304

402 MDLRFQVLETASYNGVLIWKIRYKRRKOAVMKTLSLQSPFYTGFGYKMCARVYLN 461

Db 305 -----GSDGVLIWKIGSYGRDLQAKKAPNLECSPPAFYHNKYGKQYQAVFANL 353

462 GDGNGKTHLSLFVYINAGEEDALLPWFPRKQVYVLTMLMDG-----SSRRHLDAPDPDN 517

Db 354 GNGSGEGTHLSLVIRVLPGAFNDLLEMPFARVTSLLDSDGLAKPKQHVTFEFPDPN 413

518 SSSFKRP-----TGEMNIASGCPVFAQVLENGTYIKDDTIFIKVIVDT 561

Db 414 WKNFQKGTWRGSLDESSLGFGYPRKFTISHODIKRNVIRDDAVFIRAAVE 463

RESULT 10

571821

probable interleukin 1 signal-transducing protein TRAF6 - human

C:Species: Homo sapiens (man)

C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 02-Sep-2000

C:Accession: 571821; S78550

R:Cao, Z.; Xiong, J.; Takeuchi, M.; Kurama, T.; Goeddel, D.V.

Nature 383, 443-446, 1996

A:Title: TRAF6 is a signal transducer for interleukin-1.

A:Reference number: 571821; MUID:96434892; PMID:8637778

A:Accession: 571821

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-522 <CAO>

A:Cross-references: EMBL:U08798; NID:g1732425; PIDN:AAB38751.1; PID:g1732426

R:Cao, Z.; Xiong, J.; Takeuchi, M.; Kurama, T.; Goeddel, D.V.

submitted to the EMBL Data Library, October 1996

A:Reference number: 578550

A:Accession: 578550

A:Molecule type: mRNA

A:Residues: 1-275; 'A', 277-522 <CAO>

A:Cross-references: EMBL:U08798; NID:g1732425; PIDN:AAB38751.1; PID:g1732426

C:Genetics:  
A:Gene: TRAF6  
C:Function:  
A:Description: activates transcription factor NF-kappa-B in response to interleukin-1  
A:Note: Interleukin-1 induces the association of TRAF6 with the IRAK serine/threonine kinase  
C:Superfamily: CARD receptor-associated protein CARD-1; RING finger homology  
C:Keywords: signal transduction, zinc finger  
P:66-114/Domain: RING finger homology <RRR>

Query Match	18.48;	Score 552;	DB 2;	Length 522;
Best Local Similarity	36.79;	Prod No. 10-24;		

[illegible]

RESULT 11  
T22238  
hypothetical protein F45G2.6 - *Caenorhabditis elegans*  
C:Species: *Caenorhabditis elegans*  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 02-Sep-2000  
C:Accession: T22238  
R:Lindsay, S.  
submitted to the EMBL Data Library, March 1997  
A:Reference number: Z19535  
A:Accession: T22238  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule type: DNA  
A:Residues: 1-509 <WLL>  
A:Cross-references: EMBL:Z93382; PIDN:CAE07615.1; GSPDB:GN00021; CESP:F45G2.6  
A:Experimental source: clone F45G2  
C:Genetics:  
A:Gene: CESP:F45G2.6  
A:Map position: 3  
A:Introns: 94/2; 119/3; 201/3; 223/3; 249/1; 277/3; 300/3; 327/3; 360/1; 395/3; 448/3  
C:Superfamily: Cb40 receptor-associated protein CAP-1; RING finger homology  
C:61-107/Domain: RING finger homology <RNN>

Query Match	17.4%;	Score 522.5;	DB 2;	Length 509;
Best Local Similarity	26.1%;	Pred. No. 5.1e-23;		
Matches 136;	Conservative 69;	Mismatches 188;	Indels 129;	Gaps 12

```

0Y 53 CEKHLVLCSPKQTECGHRCRPECSCMALLSSSPKCTACQCESTYVKDVFENDKREBELLA 112
Db 65 CPICEQALRDPLKLNCHDHHYRCQCFEN--ENRPGACACQITQIPELCOQDRAKOKOJILA 122
0Y 113 LQIYERNESRCAEOLTLGHLLHVLKNDCHFE-ELPCVRDCKEKKVLRKJLDHVEKACK 171
Db 123 LPVYOTFEFFSSCGPMDQGLTGTLHDHL-SECTIFKSSLKEK--CGRQPAKNDLEKHHRAK-CE 178
0Y 172 YREATCSCKSQVPMIALQKHEDTDCPCVYVVCSPHKCSVQTLRLSELSAHLSECVNAPST 231
Db 179 LNRACVSCFNKTRI RSDRDERHPT-CPQVIITSCFGQGLDRDRLEIEMHACPCBPVWDV 237
0Y 232 CSFKRYGCVFQGTMOQIKAHFASAVOHVNLKEMSNSELEKTVSLQNESVEKKNKSIQSL 291
Db 238 CPFPVYGTCTFPAKGESIEOHLSDPEFRLHMYLWLTDELTIDELGAYEJLM----- 283
0Y 292 HNOJCSFEILERQKEMLRNNESKILHLQNVIDSOAKELKEDLKEIRPPRONNEEADSMK 351
Db 284 -----ERMGSFENDQTRIL-----SAALTCTEM----- 307
0Y 352 SSVESLQNRVTELESVDKSAGQVAVARNTGLLESQLSRHQDLVYDIRLADMLRFOVLE 411
Db 308 ----- 307
0Y 412 ASYNGVLWIKTRIDYKRRRQEAVMGKTLISLYQSPFYTGFGYKMCARVYIANGDMGKTHL 471
Db 308 --FGPOLITIDKIQQRTNEAKSGADDTIFESVPFMSHREGYKMMACACLEFGDSSAGKSI 365
0Y 472 SLFVIRMGEDLALLPMPFPQKTYLIMLDGQ-----SKRHGDAFKDPDPMSSSKKAPT 525
Db 366 SLVYLLLKGEFDPLTEMPFHRRAIKISLLDNRPREDRVNTTYVIDRKLKANKEFLAPBR 425
0Y 526 GEMNIASGCPVFAQVOTLENGTYIKDQTIPIKVIYVPSD-LP 566
Db 426 GERMAAFGSSFCSLAILQ--YKDDKTYQVDVDRCELP 465

```

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RESULT 12
A29361
D617 protein - slime mold (Dictyostellium discoideum)
C:Species: Dictyostellium discoideum
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 29-Oct-1999
C:Accession: A29361
R:Driscoll, D.M.; Williams, J.G.
Mol. Cell. Biol. 7, 4482-4489, 1987
A:Title: Two divergently transcribed genes of Dictyostellium discoideum are cyclic AMP
A:Reference number: A29361; MUID:88142840; PMID:2830496
A:Accession: A29361
A:Molecule type: DNA
A:Residues: 1-458 <DRI>
A:Cross-references: GB:M18106; NID:g167729; PIDN:AAA33192.1; PID:g167730
:Keywords: DNA binding; zinc finger

```

Query Match: 6.7%; Score 201; DB 2; Length 456;  
 Best Local Similarity 20.1%; Pred. No. 0.00019;  
 Matches 115; Conservative 77; Mismatches 174; Indels 206; Gaps 28;

QY 194 DTDCPCVAVSCPHKCSVOTLLRSELSEAHSECYNAPSTCSFKRYGCVGOSTNOOIAHEA 253  
 DB 196 KT-CPMPYIDSCGSCVKIERKSIIDHENDCCNTQIPCKYFEQGC----- 240  
 QY 254 SSAYOHVNLKEMNSLEKAVSLQNSVEKNSIOSLHNOICSELEIEROKEMLRNNE 313  
 DB 241 -----KVEKRSELQN----- 251  
 QY 314 SKILHQRVIDSQAEKELDEKIRPFROMWEADSKSSVESIQNRTELESVDKSAQO 373  
 DB 252 -----HLEEV-----MHQNV-----NGILIEKLTQV-----GQ 275  
 QY 374 VARNITGLLESOLSRHDD-----LSVHDRILADMDIRFOYLETA-----SYNGVL-ITKIR 423  
 DB 276 SKKT-----HDETLKRIEDLSLYIKFSDACKLKVLPKALDICSNGYRKNKWTIS 325  
 QY 424 DY-----KRRQEAVMGKTTLSLYOPFTYGFYKMCARVYLNDGKNGKTHLSLFVFI- 477  
 DB 326 NISSVASKLMLCQALSSPMLSTLSHF-----QVC--YPRKGD--ENKEYISLYLRVN 374  
 QY 478 -----MRGEYDALLPWPFRQKVTLMMDGSSRRHLGDAFKPDNSSSEKFKPTGEMNI 530  
 DB 375 NIEEPNSLKVEXSFTL-----VNVLDKSKSITKED-----KKRVTISSE 414  
 QY 531 ASGCPVFAQTVL--ENGTIKDITFIKIVY 560  
 DB 415 GWGKGFLLSDLINKENGLMSNDKLLIETIY 446

## RESULT 13

hypothetical protein T1217.7 [imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: B96692  
 R:Thellogis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 Jensen, N.F.; Hughes, B.; Hultzer, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maltli, R.; Marziani,  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: B96692  
 A:Status: Preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-313 <STO>  
 A:Cross-references: GB:AE005173; NID:g11054583; PIDN:ANG27858.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: T1217.7  
 A:Map position: 1

## Query Match

Best Local Similarity 29.0%; Pred. No. 0.0045;  
 Matches 60; Conservative 23; Mismatches 93; Indels 31; Gaps 8;

QY 49 DRYKCEKHLVLCSP-KOTECGHRPCESCMAALLSSSEFKTACQESYKDKVFNDCCK 107  
 DB 40 DLIDPCICHAHTSPFQCDNCHICSSCCTLRN---KCPSCALPIGN---FRSRIME 92  
 QY 108 RETLALQIYCRNESCACOLILGHLVHLKNDCHFEELPCVRPOCKEVLKRDJRDH-- 165  
 DB 93 RVEAVAVVCPVKKHGTCKEFSYKELIHEK--DCRFALCYCAPKCNISGVYKDLYSHFY 151  
 QY 166 VEKACRYRATSCSHCK-----SOVPALALQKHEDTDCPCVVVSCPHKCSV 210  
 DB 152 VNHVYDWNIGGNGFAGWLRISEKILVQYGGPLIANVQCKREKNGVNVVTCIAPCAP 211  
 QY 211 QTLNSELSEAHUS--ECVNAAPTSCSK 235

DB 212 GV---GELSELSYKPKMGCNSTMMFK 235

## RESULT 14

estrogen-responsive finger protein - mouse  
 I49642  
 C:Species: Mus musculus (house mouse)  
 C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999  
 C:Accession: I49642  
 R:Orlino, A.; Inoue, S.; Ikeda, K.; Noji, S.; Muramatsu, M.  
 J. Biol. Chem. 270, 24406-24413, 1995  
 A:Title: Molecular cloning, structure, and expression of mouse estrogen-responsive fl  
 A:Reference number: I49642; MUID:96025835; PMID:7592654  
 A:Accession: I49642  
 A:Status: Preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-634 <RES>  
 A:Cross-references: GB:U63902; NID:g1088466; PIDN:BA09941.1; PID:g1088467  
 C:Superfamily: RING finger homology  
 C:Keywords: zinc  
 F:9-59/Domain: RING finger homology <RING>

## Query Match

Best Local Similarity 18.7%; Pred. No. 0.07;  
 Matches 75; Conservative 69; Mismatches 130; Indels 128; Gaps 17;

QY 49 DRYKCEKHLVLCSPKOTECGHRPCESCMAALLSSSP--KCTACQESI-VKDKVFKDN- 104  
 DB 9 EELSCSYCLELKEPVTYTPGHNFTSCUDETWVVOGPPKPCQCKVQVPRQLOKNTV 68  
 QY 105 -CCRE-----ITALQIYCRNESCACOLILGHLVHLKN 139  
 DB 69 MCANVEQFLAEGARPVDDWTPPARFSASATQVACDH---CLTEIAVKTCIACMAS 124  
 QY 140 DC-----HFEELPCVRPOCKEVLKDLRDHFKAC---KYREATCSHCKSQVPMIL 189  
 DB 125 FCEHLELPHDS-----PACQDHLQSPILRDLRRCKTOHNRKEFCP----- 168  
 QY 190 QKHEDTDCPCVAVSCPHK-CSVOTLLRSELSEAHSECYNAPSTCSFKRYGCVGOSTNOOI 248  
 DB 169 ---EHGICICHICLVEIKTCSPTTL--SQASADL----- 197  
 QY 249 KAHBASAVOHVNLKEMNSLEKAVSLQNSVEKNSIOSLHNOICSELEIEROKEM 308  
 DB 198 -----EYKLRNKLTIMHSHNGATKALEDVRSQOOCVQDSMKRMEQ 229  
 QY 309 LRNNEKILHQRVID---SQAEKLELDEK-----RPFROMWEADSKSSVES 356  
 DB 240 LR---QETMEKAVIDAETLSLRLEKEERKRYGKDTIYQVLVKKSKMOKLAEVEL 296  
 QY 357 LQNRTELESVDKSA--GOVARNITGLLESOLSRHDDMLSVH 395  
 DB 297 IMDKGDEFLEKAKAKLGESTKRVYIPKIDLD-HDLIMGIY 337

## RESULT 15

A43906  
 nuclear phosphoprotein knf7 - African clawed frog

C:Species: Xenopus laevis (African clawed frog)  
 C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 11-Jan-2000  
 C:Accession: A43906; S27947  
 R:Reddy, B.A.; Kloc, M.; Ecklin, L.  
 Dev. Biol. 148, 107-116, 1991  
 A:Title: The cloning and characterization of a maternally expressed novel zinc finger  
 A:Reference number: A43906; MUID:92038424; PMID:1936552  
 A:Accession: A43906  
 A:Molecule type: mRNA  
 A:Residues: 1-609 <RED>  
 A:Cross-references: EMBL:M63705; NID:g214914; PID:g214915  
 A:Note: sequence extracted from NCBI backbone (NCBIIN:64515, NCBIIP:64520)  
 C:Genetics:  
 A:Gene: knf7  
 C:Superfamily: Xenopus nuclear phosphoprotein knf7; RING finger homology

C;keywords: DNA binding; nucleus; phosphoprotein; zinc finger  
F;141-190/Domain: RING finger homology <RNG>

Query Match 5.1%; Score 152.5; DB 2; Length 609;  
Best local Similarity 20.7%; Pred. No. 0.16;  
Matches 69; Conservative 41; Mismatches 109; Indels 115; Gaps 12;

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QY 49 DKYCKECHLVLCSPKQTECGHNFCECM-AALLSSSPKCTACQESIYKDFKDNCK 107
   : : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 141 EELTCLCEVELFKDPYVACGHNFCRSCIDKAMEGGSFACPECRSITDRK----- 192
QY 108 REILALQITCRNBSRGCALQLTGLHLVHLKNDCHFEEELPCVRPDCKEVLKKDLRDHYE 167
   : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 193 -----YTINRYLANIA-----KKAACTPVTVPVEKTRP-----LE 222
QY 168 KACKYREATCSHCKSQVPMIALQKHEDTDCPCVVVSCPHKCSVQTLL-----RSEI 218
   : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 223 KCEHDERLKLCK-----DDGTLSCVICRDSLKHASHNPLPILDVAVGYREEL 271
QY 219 SAHLSECVNAPSTCSFKRYGCVFGTNOQIKAHEASSAVOHVNLKEMNSLEKKVSLIQ 278
   : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 272 SA-----IVAPLEASLK-----VTEQLSSEQSDKITEQ----- 299
QY 279 NESVEKKSIOSLHNOICFELIEIEROKEMLNNSKILHLQRYIDSOAEKLELDKEIR 338
   : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 300 -----NKNMSQYKEHITS--EFELKHLKFLRERREKEL-----EQLKEQGENLL 340
QY 339 PFRON-----WEADSMKSSVESLONRVTELESV 367
   : : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 341 TEMENNLYVMQESQDAIKKTIISLAKERMEDTDSI 374

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Search completed: December 19, 2002, 14:55:59  
Job time : 25 secs